

Reviewer Report

Title: Enhancing Bovine Genome Annotation Through Integration of Transcriptomics and Epi-Transcriptomics Datasets Facilitates Genomic Biology

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Reviewer Comments to Author:

This is an amazing study including huge annotation work for cattle genome. It identified 171,985 high quality unique transcripts with 69% of them un-annotated. Moreover, genes'/transcripts' diversity among tissues, different development stages were compared and their similarities with other species were analyzed. This updated the known knowledge of cattle transcriptome, and will be significant for understanding the regulation mechanism of body traits. This manuscript was recommended to be accepted after a minor revision.

1. Maybe a flow chart including samples (their number), methods, etc will be helpful for authors to understand of the outline of this study when it supplied so much information. Besides, subheadings for the Results part needs to be detailed to supply a clear aim or result, for example, "Transcript level analyses".

2. Predicted un-annotated genes and transcripts were highly supported by independent Pacific Biosciences single molecule long-read isoform sequencing (PacBio Iso-Seq), Oxford Nanopore Technologies sequencing (ONT-seq), Illumina high-throughput RNA sequencing (RNA-seq), Whole Transcriptome Termini Site Sequencing (WTTS-seq), RNA Annotation and Mapping of Promoters for the Analysis of Gene Expression (RAMPAGE), chromatin immunoprecipitation sequencing (ChIP-seq), and Assay for Transposase-Accessible Chromatin using sequencing ATAC-seq) data.

How did this validation applied using those different datasets? Which one was treated as standard, or were they validated mutually by overlapping? Detail information is needed to supply to help others to refer this study when they compare with their own datasets. Standard work flow will help the cattle study to go faster, and this will be a very important contribution.

3. Testis showed the highest number of expressed genes with observed transcripts compared to other tissues. Fetal brain and fetal muscle tissues showed the highest number and percentage of non-coding genes compared to that observed in other tissues

When evaluated the gene/transcript number for different tissues, were the numbers corrected by the sequencing depth/the sample number of different tissues? How to define the testis including the highest number of expressed genes? Is there any potential interesting biological mechanism for this phenomenon?

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

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Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Choose an item.

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